#24

1600

RAW SEQUENCE LISTING   DATE: 04/24/2002
PATENT APPLICATION: US/09/509,283B   TIME: 09:14:52 ENTERED

Input Set : A:\7853215999.txt
Output Set: N:\CRF3\04242002\I509283B.raw

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 3 <110> APPLICANT: Kroczek, Richard
 5 <120> TITLE OF INVENTION: Anti-human T-cell costimulating monoclonal antibodies
 7 <130> FILE REFERENCE: 7853-215-999
 9 <140> CURRENT APPLICATION NUMBER: 09/509,283B
10 <141> CURRENT FILING DATE: 2000-08-11
12 <160> NUMBER OF SEQ ID NOS: 5
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2641
18 <212> TYPE: DNA
19 <213> ORGANISM: 8F4
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: 68..667
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27 ggcaaac atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc     109
28         Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg
29          1               5                  10
30 att aaa gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg     157
31 Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met
32  15              20                  25                  30
33 ttt ata ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac     205
34 Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp
35              35                  40                  45
36 att gtc cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc     253
37 Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu
38              50                  55                  60
39 tgc gat ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag     301
40 Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys
41              65                  70                  75
42 agt ctg aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt     349
43 Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe
44      80                  85                  90
45 ttt cta tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac     397
46 Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn
47  95                 100                 105                 110
48 cta tca att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga     445
49 Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly
50             115                 120                 125
51 tat ttg cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg     493
52 Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp
53             130                 135                 140
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54 tta ccc ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc       541
55 Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys
56         145                 150                 155
57 ata ctt att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac       589
58 Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His
59     160                 165                 170
60 gac cct aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa       637
61 Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys
62 175                 180                 185                 190
63 aaa tct aga ctc aca gat gtg acc cta taa tatggaactc tggcacccag        687
64 Lys Ser Arg Leu Thr Asp Val Thr Leu
65                 195
66 gcatgaagca cgttggccag ttttcctcaa cttgaagtgc aagattctct tatttccggg    747
67 accacggaga gtctgactta actacataca tcttctgctg gtgttttgtt caatctggaa    807
68 gaatgactgt atcagtcaat ggggatttta acagactgcc ttggtactgc cgagtcctct    867
69 caaaacaaac accctcttgc aaccagcttt ggagaaagcc cagctcctgt gtgctcactg    927
70 ggagtggaat ccctgtctcc acatctgctc ctagcagtgc atcagccagt aaaacaaaca    987
71 catttacaag aaaaatgttt taaagatgcc aggggtactg aatctgcaaa gcaaatgagc   1047
72 agccaaggac cagcatctgt ccgcatttca ctatcatact acctcttctt tctgtaggga   1107
73 tgagaattcc tcttttaatc agtcaaggga gatgcttcaa agctggagct attttatttc   1167
74 tgagatgttg atgtgaactg tacattagta catactcagt actctccttc aattgctgaa   1227
75 ccccagttga ccattttacc aagactttag atgctttctt gtgccctcaa ttttcttttt   1287
76 aaaaatactt ctacatgact gcttgacagc ccaacagcca ctctcaatag agagctatgt   1347
77 cttacattct ttcctctgct gctcaatagt tttatatatc tatgcataca tatatacaca   1407
78 catatgtata taaaattcat aatgaatata tttgcctata ttctccctac aagaatattt   1467
79 ttgctccaga aagacatgtt cttttctcaa attcagttaa aatggtttac tttgttcaag   1527
80 ttagtggtag gaaacattgc ccggaattga aagcaaattt attttattat cctattttct   1587
81 accattatct atgttttcat ggtgctatta attacaagtt tagttctttt tgtagatcat   1647
82 attaaaattg caaacaaaat catctttaat gggccagcat tctcatgggg tagagcagaa   1707
83 tattcattta gcctgaaagc tgcagttact ataggttgct gtcagactat acccatggtg   1767
84 cctctgggct tgacaggtca aaatggtccc catcagcctg gagcagccct ccagacctgg   1827
85 gtggaattcc agggttgaga gactcccctg agccagaggc cactaggtat tcttgctccc   1887
86 agaggctgaa gtcaccctgg gaatcacagt ggtctacctg cattcataat tccaggatct   1947
87 gtgaagagca catatgtgtc agggcacaat tccctctcat aaaaaccaca cagcctggaa   2007
88 attggccctg gcccttcaag atagccttct ttagaatatg atttggctag aaagattctt   2067
89 aaatatgtgg aatatgatta ttcttagctg gaatattttc tctacttcct gtctgcatgc   2127
90 ccaaggcttc tgaagcagcc aatgtcgatg caacaacatt tgtaacttta ggtaaactgg   2187
91 gattatgttg tagtttaaca ttttgtaact gtgtgcttat agtttacaag tgagacccga   2247
92 tatgtcatta tgcatactta tattatctta agcatgtgta atgctggatg tgtacagtac   2307
93 agtactgaac ttgtaatttg aatctagtat ggtgttctgt tttcagctga cttggacaac   2367
94 ctgactggct ttgcacaggt gttccctgag ttgtttgcag gtttctgtgt gtggggtggg   2427
95 gtatggggag gagaaccttc atggtggccc acctggcctg gttgtccaag ctgtgcctcg   2487
96 acacatcctc atccccagca tgggacacct caagatgaat aataattcac aaaatttctg   2547
97 tgaaatcaaa tccagtttta agaggagcca cttatcaaag agattttaac agtagtaaga   2607
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101 <211> LENGTH: 199
102 <212> TYPE: PRT
103 <213> ORGANISM: 8F4
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109 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
110             20                  25                  30
112 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
113             35                  40                  45
115 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
116         50                  55                  60
118 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
119 65                  70                  75                  80
121 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
122             85                  90                  95
124 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
125             100                 105                 110
127 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
128         115                 120                 125
130 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
131     130                 135                 140
133 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
134 145                 150                 155                 160
136 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
137             165                 170                 175
139 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
140             180                 185                 190
142 Arg Leu Thr Asp Val Thr Leu
143             195
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 17
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerate
oligonucleotide
W--> 153 <221> NAME/KEY: misc_feature
154 <222> LOCATION: 3, 9 , 15
155 <223> OTHER INFORMATION: n = a, t, g, or c
W--> 157 <400> 3
W--> 158 mgnctsacng aygtnac                                            17
160 <210> SEQ ID NO: 4
161 <211> LENGTH: 17
162 <212> TYPE: DNA
C--> 163 <213> ORGANISM: Artificial
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerate
oligonucleotide
W--> 168 <221> NAME/KEY: misc_feature
169 <222> LOCATION: 3, 9 , 15
170 <223> OTHER INFORMATION: n = a, t, g, or c
W--> 172 <400> 4
W--> 173 mgnytdacng aygtnac                                            17
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Input Set : A:\7853215999.txt
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175 <210> SEQ ID NO: 5
176 <211> LENGTH: 7
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <220> FEATURE:
181 <221> NAME/KEY: SITE
182 <222> LOCATION: 1
183 <223> OTHER INFORMATION: Xaa = Unknown amino acid
185 <400> SEQUENCE: 5
186 Xaa Arg Leu Thr Asp Val Thr
187 1               5
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